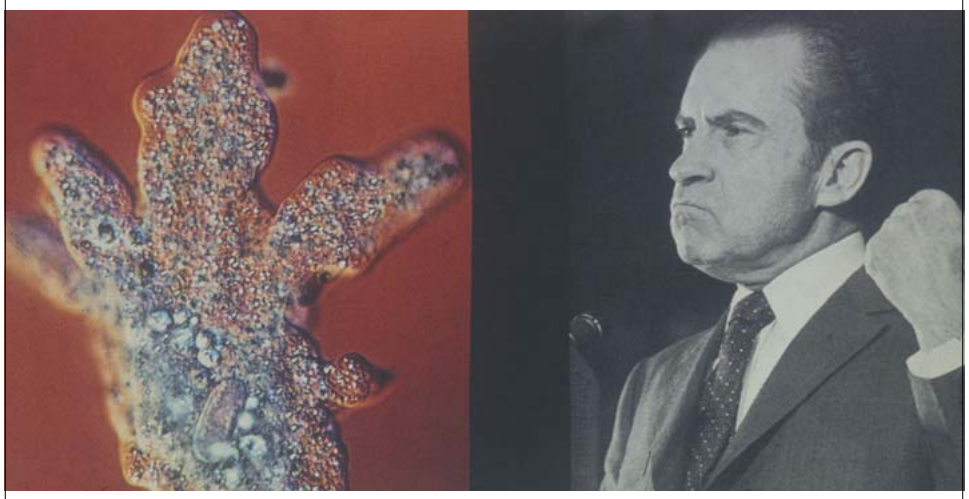
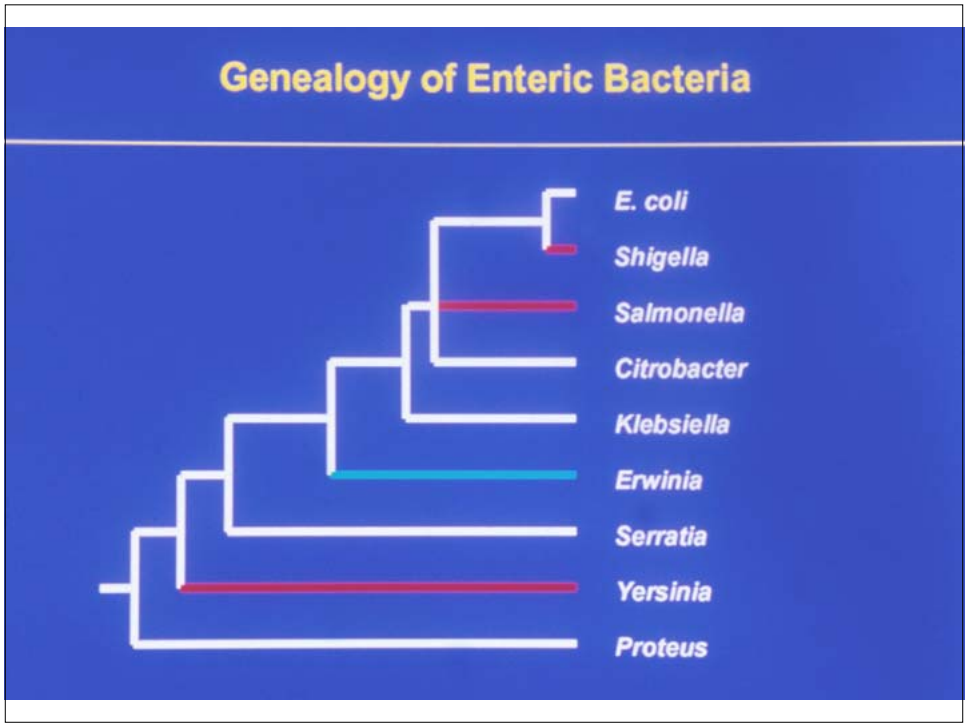
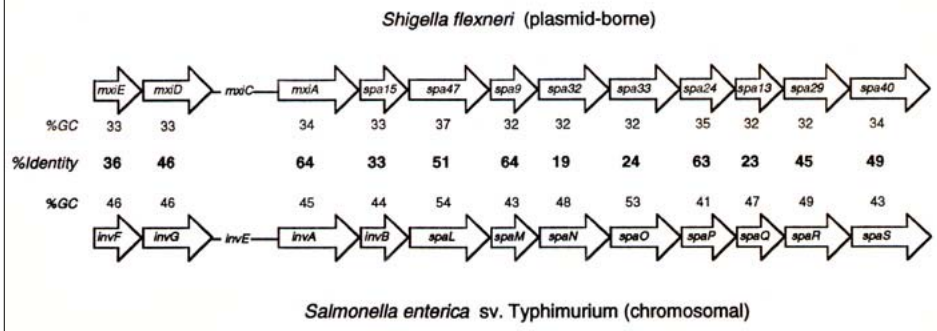



Genealogy of Enteric Bacteria
E. coli
Shigella
Salmonella
Citrobacter
Klebsiella
Erwinia
Serratia
Yersinia
Proteus

WHAT MAKES *SALMONELLA* PATHOGENIC?

1. The presence of *Salmonella*-specific sequences encoding virulence functions.
2. Allelic variation in the same set of genes.
3. Differential regulation of the same set of genes.
4. The absence of a "repressor of virulence functions" from the *Salmonella* genome.



PATHOGENICITY ISLANDS

. Segments of the chromosome harboring large clusters of virulence genes

. Present in pathogenic strains but absent or sporadically distributed in related non-pathogenic species

. Typically have a G+C content different from that of the rest of the chromosome

. Often associated with tRNA genes and/or mobile genetic elements at their boundaries

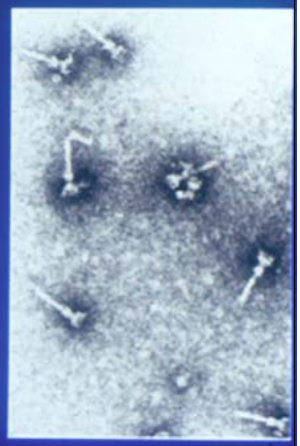
TYPE III SECRETION SYSTEMS

. Specialized protein export machineries used by Gram-negative pathogens and symbionts to deliver toxic proteins into the host cell cytosol

. Require a large number of accessory proteins to export substrates across both the inner and outer membranes

. Secreted substrates lack typical Sec-dependent signal sequences

. Host signals activate secretion and delivery of virulence proteins into host tissues

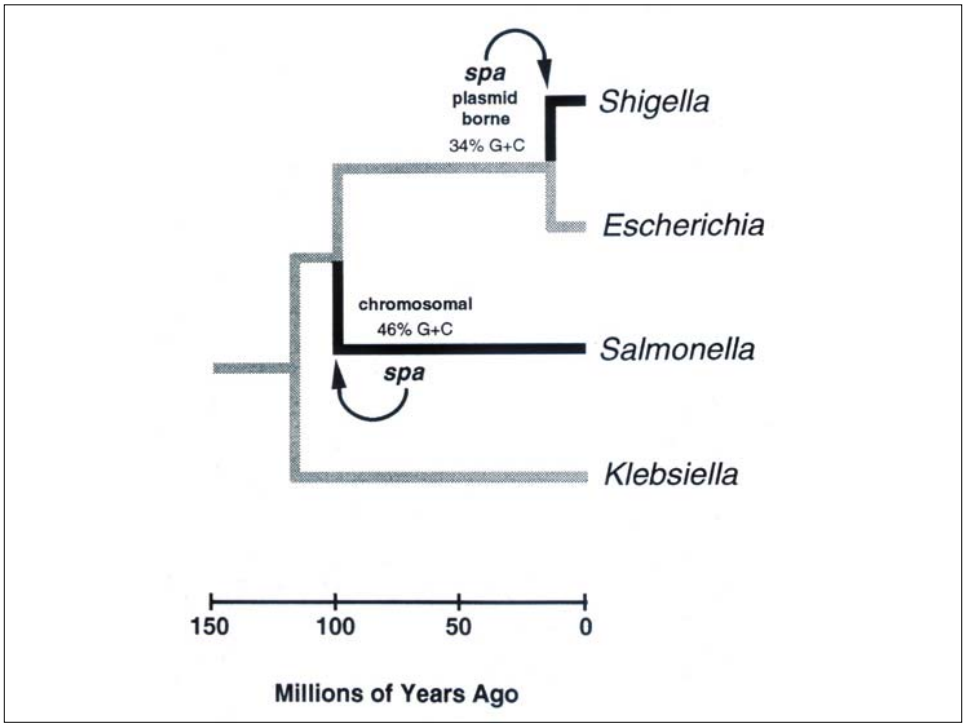


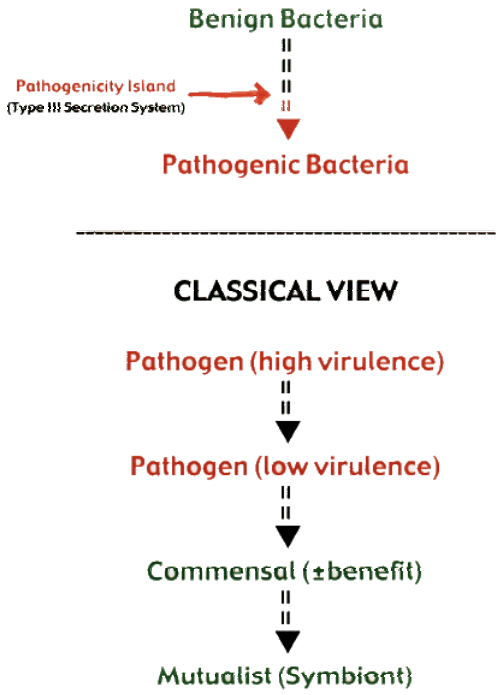
Kubori, et al, 1998

Homologues of the Salmonella Invasion Genes in Other Bacterial Pathogens

Salmonella	*Shigella*	*Yersinia*	EHEC	Plant pathogens*	Flagellar
InvA	MxiA	LcrD	SepA	HrpO/HrcV	FlhA
InvG	MxiD	YscJ	SepC	HrpA/HrcC	—
SpaL	Spa47	YscN	SepB	HrpE/HrcN	FliI
SpaO	Spa33	YscQ	—	HrpQ/HrcQ	FliN
SpaP	Spa24	YscR	SepI	HrpT/HrcR	FliP
SpaQ	Spa9	YscS	SepH	HrpU/HrcS	FliQ
SpaR	Spa29	YscT	SepG	HrpC/HrcT	FliR
SpaS	Spa40	YscU	SepF	HrpN/HrcU	FlhB
PrgH	MxiG	—	—	—	—
PrgK	MxiJ	YscJ	SepD	HrpI/HrcJ	FliF
InvE	MxiC	LcrH	SepE	—	—
SpaK	Spa15	—	—	—	FliH

* includes *Pseudomonas*/*Ralstonia solanacearum*, *Pseudomonas syringae*, *Xanthomonas campestis*, *Erwinia spp.*

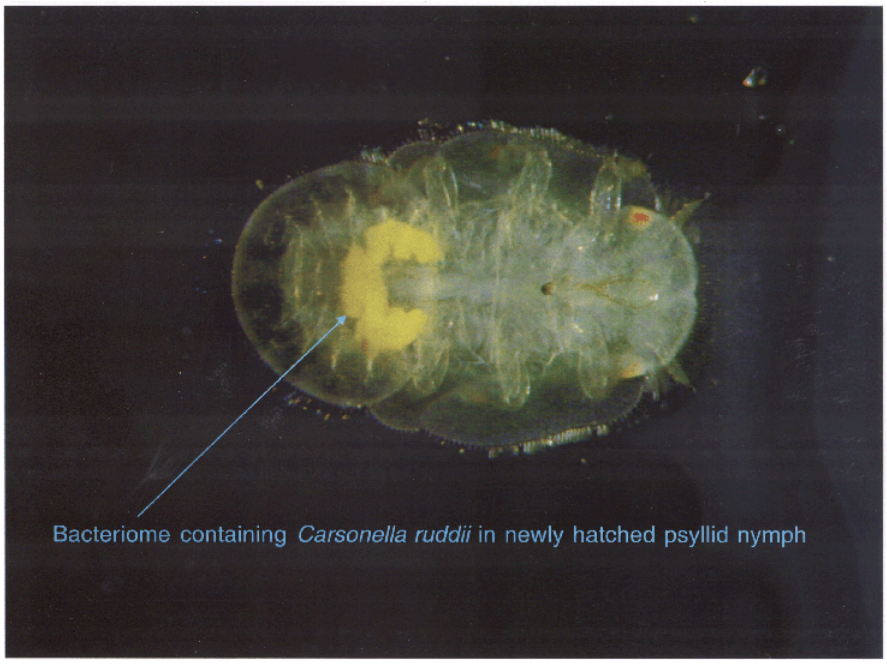




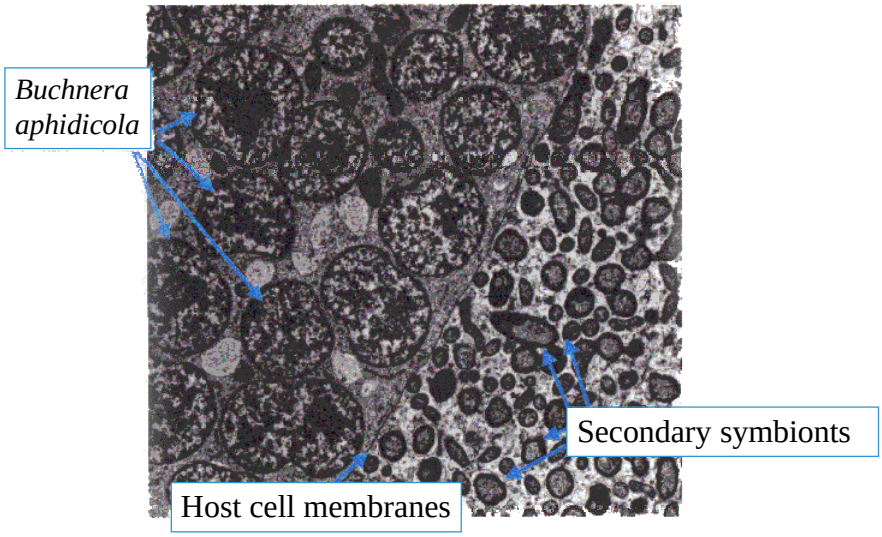
Bacterial Symbionts of Insects

- Occur in a very broad range of insects (P. Buchner, 1965)
- Bacteria required for insect survival ('primary' endosymbionts)
- Make up for deficiencies in the host diet.
- Reside within specialized host organs (bacteriomes, mycetomes)
- Strict vertical inheritance (eggs infected by maternal symbionts)

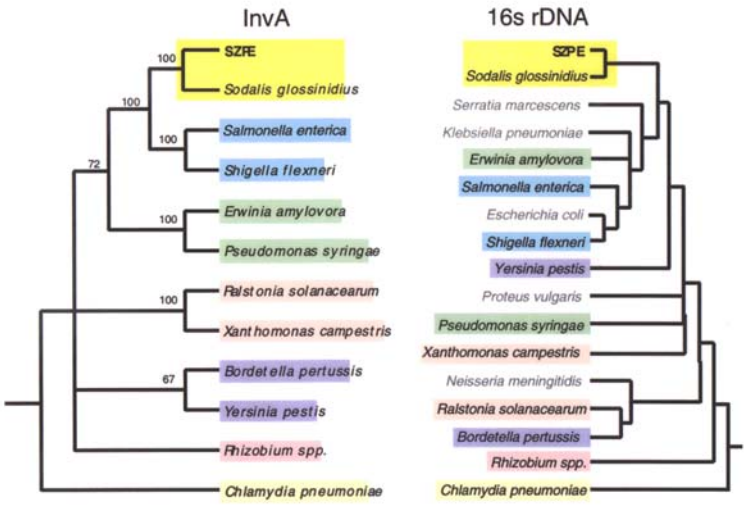
This is a switch from 'secondary' symbionts (and pathogens) that are not required by the host and transmitted *horizontially*



Intracellular bacterial symbionts in pea aphids



inv/16S rDNA phylogenies



Expression of the *inv*/*spa* genes *in vivo*

- *Sitophilus* spp. are holometabolous insects
- larvae (0-16d) → pupae (16-21d) → adult (>24d)

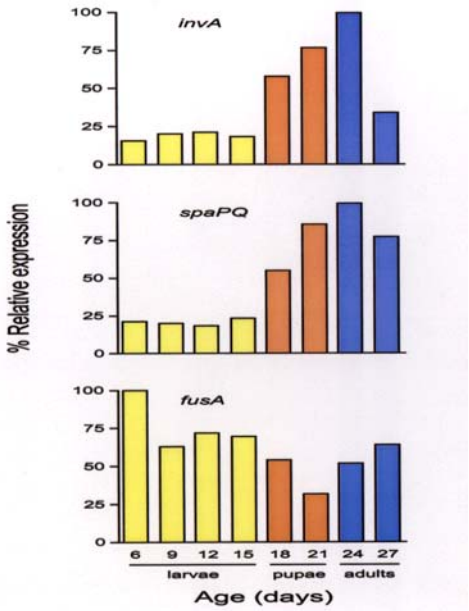
REINFECT NEW BACTERIOME

→Synchronized *Sitophilus* reproduction by allowing adults to mate and oviposit in maize over 24h

-Prepared RNA from isolated mycetomes at time intervals following oviposition

(BACTERIOMES)

-Performed RT-PCR analysis using Lightcycler



Conclusions:

1. Type III secretion system acquired by ancestor of this symbiont prior to establishing obligate relationship with host.
2. Type III secretion system in symbiont homologous to that used for host cell invasion by bacterial pathogens.
3. Type III secretion system has been adopted to maintain obligate symbiosis (to recolonize new bacteriome).
4. First molecular genetic evidence for an apparatus used by pathogens to aid in the conversion to mutualism.